Heridity and Epigenetics in Systemic Lupus Erythematosus

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Abstract

Systemic lupus erythematosus (SLE) is an autoimmune, connective tissue disease of unknown aetiology where both genetic and environmental risk factors contribute moderately to an increased risk. However, important parts of the picture are still missing, which may at least in part be explained by epigenetic mechanisms that regulate gene expression without altering the DNA sequence, where DNA methylation is the key player.

With the present PhD project we wish to elucidate hereditary and epigenetic factors that may participate in the pathogenesis of SLE. Firstly, we undertake to investigate the familial aggregation of SLE in a national register-based study to answer the question of what is the risk of SLE patients' relatives being diagnosed with similar disease. Secondly, we undertake a case-control study of twin pairs where at least one has SLE and a separate sample of SLE patients compared to healthy controls to identify epigenetic areas of interest, i.e. differentially methylated genes. Thirdly, through clinical evaluation and blood samples we will investigate such differentially methylated genes in separate immune cell populations in SLE patients compared to controls and the DNA methylation pattern will be related to disease activity and disease manifestations. Thus, the project seeks to identify new areas in the human epigenome that may be correlated to SLE in the hope of finding new targets for therapy and biomarkers for SLE identification.